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New heights and horizons in fostering proteomics in central and eastern Europe

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6th Central and Eastern European Proteomic Conference

Budapest, Hungary, 14–17 October 2012

The annual Central and Eastern European Proteomic Conference can be considered as the bedrock of proteomics in central and eastern Europe and, since its creation, has seen an incredible growth in proteomics. The term 'Central and Eastern European Proteomic Conference' (CEEPC) was coined by the founder members of this series of conference including Josef Chmelik (1953–2007), Suresh Jivan Gadher and Hana Kovarova, over discussions about the apparent lack of visibility of proteomics in central and eastern Europe, as well as infrequent meetings and almost total lack of international collaborations. With trepidation, the 1st Central and Eastern European Proteomic Conference was organized in Prague in 2007 with resultant huge success. The intervening years saw the CEEPC grow and expand, and it now represents a cradle of proteomics interactions in and around central and eastern Europe, nicely linking it to the whole world. The 6th CEEPC in Budapest was attended by 150 participants and excelled once again at promoting proteomics at the highest level.

The cornerstone in the evolution of the Central and Eastern European Proteomic Conference (CEEPC) was the friendship between scientists from Czech Republic, Russia, Austria, Hungary, the UK, Canada and the USA. It all began with invitations to such researchers and friends to visit Prague, participate in scientific discussions and to share ideas in a friendly and informal environment over good Czech beer or Moravian wine. Subsequent intense work by the members of the Czech Proteomic Society board, namely Hana Kovarova (Czech Academy of Sciences, Libeň, Czech Republic), Josef Chmelik (Czech Academy of Sciences, Brno, Czech Republic) and invited scientific advisor Suresh Jivan Gadher (Life Technologies, MD, USA), laid the foundation for the birth of the 1st CEEPC organized in Prague on 29–31 October 2007, jointly with the 3rd Czech Proteomics Conference [1,2]. Sadly, that same year, Chmelik, who was a stalwart member of the founder team, suddenly passed away. Chmelik, who had devoted his entire life to proteomics and glycomics, had a vision to create a dynamic and integrated research community inclusive of all cultural societies [3]. This vision was propagated by Kovarova

and Gadher and expansion of the CEEPC was initiated by welcoming Germany, Austria and Hungary to this privileged Conference. The Scientific Advisory board was established and currently includes Kovarova and Gadher, Ales Svatos (Max-Planck Institute of Ecology, Jena, Germany), Károly Vékey and László Drahos (Chemical Research Centre, Hungarian Academy of Sciences, Budapest, Hungary) and Guenter Allmaier (University of Technology, Vienna, Austria). Recent participation by Russia and India, where there is phenomenal growth in proteomics, added to the excitement [4]. As a result, an expansive network of proteomics in central and eastern Europe stands established and thrives on mutual trust and friendship. In the authors' opinion CEEPC is one of a very few meetings undistracted by rivalry, secrecy of ideas or wrangling, and remains a friendly and relaxed forum for interaction. Rotation of the meeting's venue each year to iconic cities of the world such as Jena (Germany), Vienna (Austria), Prague (Czech Republic) or Budapest (Hungary) and the sharing of different cultures, histories, fine cuisines, wines and music adds to intertwining of 'cutting edge' research and excitement. To

this day, CEEPC's outstanding success is due to the undiminished enthusiasm of this unique group of friends, their younger researchers and participating scientists from all over the world, returning each year for this intoxicating mixture of proteomics and warm friendship. This is an ever expanding conference that stands to grow as neighboring regions come onboard to propagate this vision further.

Report

The 6th CEEPC was organized in Budapest, Hungary on 14–17 October 2012 with resounding success and followed on from the 5th CEEPC in Prague, Czech Republic the year before. High caliber expert speakers and enthusiastic participants from no less than 18 different countries attended this meeting. Cutting-edge proteomics was extensively discussed and debated, and priority was given to researchers from emerging countries as well as young students to share their results with all. The Organizing Committee, under the auspices of Vékey and Drahoš, put together a fascinating scientific and cultural program for all to enjoy. This conference offered participants both the excitement of novel proteomics as well as the buzz of Budapest with its rich culture.

With a major focus on health and glycosylation, the scientific program commenced on the 15 October with György Markovarga (Lund University, Lund, Sweden) presenting the impact of biobanking on future healthcare with automated sample processing strategy. Biobank storage of small sample volumes, where each sample aliquot can be used for a dedicated clinical analysis and end point measurement, was judged useful in the development of personalized medicine or for clinical cohort study for biomarker discovery and development. Stephen Pennington (University College Dublin, Dublin, Ireland) discussed proteomic and bioinformatic approaches to development of biomarker signatures for prostate cancer from discovery to targeted verification. Tadashi Kondo (National Cancer Centre Research Institute, Tokyo, Japan) debated cancer biomarker development and discussed gastrointestinal stromal tumor with reference to p16, which was upregulated in patients cured by surgery alone, suggesting that a single biomarker approach may help predict metastasis after surgery.

Studies on proteomic analysis of epileptic human brain – alcoholic' mobile phase by Goran Mitulović (Medical University of Vienna, Vienna, Austria) showed detection of more proteins due to increased volume of alcohol in separation phase, resulting in selective changes in peptide retention times on reversed-phase system and in MS/MS spectra. Helmut Meyer (Ruhr-Universität Bochum, Bochum, Germany) presented a talk on tissue-based proteomics as a tool for biomarker discovery, and this was followed by an excellent talk by Andreas Rizzi (University of Vienna, Vienna, Austria) who alluded to targeted proteomics approaches for monitoring cytokine secretion using ELISA assays and mass spectrometry (MS)-based targeted quantification methods with spectacular outcome. Thomas Kislinger (Ontario Cancer Institute, ON, Canada) explored the cell-surface proteome for embryo-derived stem cell lines using affinity labeling and MS. Antibodies against lineage-specific cell-surface proteins enabled

identification and isolation of specific cell populations during stem cell differentiation and reprogramming. Gadher presented a talk on 'Human follicular fluid as a cache for possible biomarkers' to address infertility and prediction of ovarian hyperstimulation syndrome in women undergoing *in vitro* fertilization. Results indicated involvement of angiogenesis and tailored chemotaxis and a set of key cytokines were also suggested for novel therapeutic intervention. This presentation was followed by Kovarova (Institute of Animal Physiology and Genetics AS CR, v.v.i., Libeň, Czech Republic), who presented a talk on the 'Neural progenitor surfaceome and secretome for transplantation research into spinal cord injury and neurological disorders' using neural progenitor cells. Cell surface capturing technology was applied to characterize surfaceome of neural progenitor cells during neuronal differentiation. Among secreted molecules, mainly chemokines of CXCL and CCL families were observed.

On day 2 the focus switched to glycoproteomics with András Guttman (University of Veszprém, Veszprém, Hungary) discussing glycosylation, and was followed by Guenter Allmaier (Vienna University of Technology, Vienna, Austria) reporting on the strong influence of glycosylation on pharmacokinetics and half-life of therapeutic glycoproteins. Allmaier described a system to express and purify the model glycoprotein erythropoietin and to analyze its *N*- and *O*-glycans by a glycomic approach applying MALDI MS. Stefan Toegel (Medical University of Vienna, Vienna, Austria) presented a very important talk on the emerging role of glycobiology in osteoarthritis, including glycan mapping and galectin function in cartilage. Toegel suggested that osteoarthritic conditions alter specific features of the glycophenotype of human chondrocytes and cartilage matrix. Resultant altered sugar code may be translated by galectin-1, which is increased in osteoarthritis and drives further degeneration of cartilage. Pavel Rehulka (University of Defense, Hradec Králové, Czech Republic) showed how analysis of protein glycosylation using a simple microgradient separation device combined off-line with MALDI-TOF/TOF MS analysis was highly informative and often used to gain a deeper insight into glycoprotein structure.

Vékey addressed difficulties associated with glycosylation studies hampered by sample preparation and analysis. An interesting protocol was presented for glycopeptide analysis where glycosylation pattern of a given glycoprotein is obtained for a glycoprotein mixture with added benefit of obtaining glycosylation pattern specific to various glycosylation sites. Anthony Gramolini (University of Toronto, ON, Canada) showed plasma membrane proteomic analysis of mouse and human cardiovascular proteins with key biological functions. This provided a pipeline of proteins to validate surface proteins in cardiomyocytes that may be critical in calcium dynamics. Mikhail Gorshkov (Russian Academy of Sciences, Moscow, Russia) in his presentation, 'Putting more orthogonality into proteomics workflow', reported on recent developments in applying the arrays of orthogonal information about the peptide and/or protein sequences in search for the method of their identifications alternative to the MS/MS.

The final day of the conference commenced with discussions on 'Clinical proteomics – from discovery to implementation' and the merits of different instrumentation in biomarker validation. Martina Marchetti-Deschmann (Vienna University of Technology, Vienna, Austria) followed with a study on *Trichoderma* species used as biological control agents against fungal pathogens, based on a direct mycoparasitic interaction of the fungus *Trichoderma* with the plant pathogenic host fungus. Bruno Domon (Luxembourg Clinical Proteomics Centre, CRP-Santé, Strassen, Luxembourg) reported on the next generation of quantitative targeted techniques based on a novel quadrupole/orbitrap instrument. The high acquisition speed, sensitivity and additional selectivity of such a hybrid mass spectrometer could facilitate qualitative and quantitative studies with quantification of biomarkers in bodily fluids. Svatos discussed 'Profiling and quantitative plant proteomics in data independent mode'. Svatos highlighted an approach for ecologically relevant quantitative proteomics, protein turnover and nitrogen flux studies under different natural conditions, suggesting that MS-based proteomics was an excellent tool for molecular-based plant biotic interactions. Tamás Janaky (University of Szeged, Szeged, Hungary) delivered an interesting talk on small peptides inhibiting the interaction of oligomeric amyloid- β peptide and the use of such peptides in rational drug design for Alzheimer's disease. Roman Zubarev (Karolinska Institute, Stockholm, Sweden) brought the proceedings of the meeting to a close with a presentation describing

the separation of polypeptides by isoelectric point focusing in electrospray-friendly solution using multiple junction capillary fractionator and related technologies for the quantification and identification of a large numbers of proteins.

Conclusion

Proteomics has promising and exciting potential across many biological and medical applications areas. This, together with the energy and enthusiasm of young generation of researchers fascinated by proteomics, may enable diverse fields such as stem cell biology, metabolomics, drug discovery and disease research to reach their end goal for many diseases affecting mankind. In keeping with tradition, the next 7th CEEPC will be held in Jena, Germany in 2013, where once again exciting advances in proteomes, proteomics and biological systems-related topics will be discussed in this vibrant city, offering local hospitality to be savored with newer challenges and deeper fascination of proteomics.

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